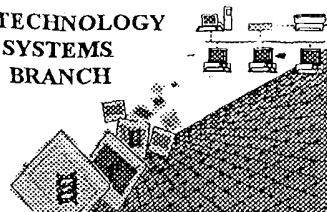


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/786,926A
Source: 1692
Date Processed by STIC: 10/10/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/2003):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/2003



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/786,926A

DATE: 10/10/2003

TIME: 10:55:39

Input Set : A:\pto.yf.txt

Output Set: N:\CRF4\10102003\I786926A.raw

3 <110> APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
 5 <120> TITLE OF INVENTION: Human and murine G-protein coupled EDG6 receptor
 6 (endothelial differentiation gene) and use of same
 8 <130> FILE REFERENCE: 101195-45
 10 <140> CURRENT APPLICATION NUMBER: US/09/786,926A
 11 <141> CURRENT FILING DATE: 2001-05-04
 13 <150> PRIOR APPLICATION NUMBER: DE 198 43 240.2
 14 <151> PRIOR FILING DATE: 1998-09-11
 16 <150> PRIOR APPLICATION NUMBER: DE 198 46 979.9
 17 <151> PRIOR FILING DATE: 1998-10-13
 19 <150> PRIOR APPLICATION NUMBER: PCT/DE 99/02871
 20 <151> PRIOR FILING DATE: 1999-09-10
 E--> 22 <160> NUMBER OF SEQ ID NOS: 416 (p.3)
 24 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

263 <210> SEQ ID NO: 5
 264 <211> LENGTH: 30
 265 <212> TYPE: DNA
 266 <213> ORGANISM: Artificial Sequence
 W--> 267 <220> FEATURE:
 268 <223> OTHER INFORMATION: Sequence of PCR Primer R1
 270 <400> SEQUENCE: 5
 E--> 272 cgg gat cgg cvt dvt sgg maa ykb vyt sgt
 275 <210> SEQ ID NO: 6
 276 <211> LENGTH: 29
 277 <212> TYPE: DNA
 278 <213> ORGANISM: Artificial Sequence
 W--> 279 <220> FEATURE:
 280 <223> OTHER INFORMATION: Sequence of PCR Primer R3
 282 <400> SEQUENCE: 6
 E--> 284 cgg gat cgg aar gyr tas ads adr ggr tt
 287 <210> SEQ ID NO: 7
 288 <211> LENGTH: 21
 289 <212> TYPE: DNA
 290 <213> ORGANISM: Artificial Sequence
 W--> 291 <220> FEATURE:
 292 <223> OTHER INFORMATION: Sequence of PCR Primer 5'hGSPRT
 294 <400> SEQUENCE: 7
 E--> 296 ttg gag cga aag acg tgc gcc
 298 <210> SEQ ID NO: 8

Does Not Comply
Corrected Diskette Needed

pp 1-3

30 ← insert cumulative
nucleotide total at right
margin of each line

29 ← insert

21 ←

RAW SEQUENCE LISTING

DATE: 10/10/2003

PATENT APPLICATION: US/09/786,926A

TIME: 10:55:39

Input Set : A:\pto.yf.txt

Output Set: N:\CRF4\10102003\I786926A.raw

```

299 <211> LENGTH: 21
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
W--> 302 <220> FEATURE:
303 <223> OTHER INFORMATION: Sequence of PCR Primer 5'hGSP1
305 <400> SEQUENCE: 8
E--> 307 agg cag aag agg atg tag cgc      21<
310 <210> SEQ ID NO: 9
311 <211> LENGTH: 21
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial Sequence
W--> 314 <220> FEATURE:
315 <223> OTHER INFORMATION: Sequence of PCR Primer 5'hGSP2
317 <400> SEQUENCE: 9
E--> 319 gcg ctc ccc tgc agt gaa gag      21<
322 <210> SEQ ID NO: 10
323 <211> LENGTH: 21
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
W--> 326 <220> FEATURE:
327 <223> OTHER INFORMATION: Sequence of PCR Primer 3'hGSP1
329 <400> SEQUENCE: 10
E--> 331 agt gac ctg ctc acg ggc gcg      21<
333 <210> SEQ ID NO: 11
334 <211> LENGTH: 21
335 <212> TYPE: DNA
336 <213> ORGANISM: Artificial Sequence
W--> 337 <220> FEATURE:
338 <223> OTHER INFORMATION: Sequence of PCR Primer 3'hGSP2
340 <400> SEQUENCE: 11
E--> 342 ctc ttc act gca ggg gag cgc      21<
345 <210> SEQ ID NO: 12
346 <211> LENGTH: 24
347 <212> TYPE: DNA
348 <213> ORGANISM: Artificial Sequence
W--> 349 <220> FEATURE:
350 <223> OTHER INFORMATION: Sequence of PCR Primer 5'mGSPRT
352 <400> SEQUENCE: 12
E--> 354 ctc acc tcg tct ggg agg gcc tgc      24<
358 <210> SEQ ID NO: 13
359 <211> LENGTH: 24
360 <212> TYPE: DNA
361 <213> ORGANISM: Artificial Sequence
W--> 362 <220> FEATURE:
363 <223> OTHER INFORMATION: Sequence of PCR Primer 5'mGSP1
365 <400> SEQUENCE: 13
E--> 367 tgg gca act ggc tgg tcc aag ctc      24<
370 <210> SEQ ID NO: 14
371 <211> LENGTH: 49

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/786,926A

DATE: 10/10/2003

TIME: 10:55:39

Input Set : A:\pto.yf.txt

Output Set: N:\CRF4\10102003\I786926A.raw

372 <212> TYPE: DNA
 373 <213> ORGANISM: Artificial Sequence
 375 <220> FEATURE:
 376 <223> OTHER INFORMATION: Sequence of PCR Primer 5'mGSP2
 378 <400> SEQUENCE: 14
 E--> 379 gcc tcg ggc cca gat cct cca ggg gtg ctg cgg acg ctg gaa atg ctg g
 383 <210> SEQ ID NO: 15
 384 <211> LENGTH: 21
 385 <212> TYPE: DNA
 386 <213> ORGANISM: Artificial Sequence
 W--> 387 <220> FEATURE:
 388 <223> OTHER INFORMATION: Sequence of 3' primer
 390 <400> SEQUENCE: 15
 E--> 392 cca cgt cct cct gcc cgc cgc 21←
 400 <210> SEQ ID NO: 16
 401 <211> LENGTH: 21
 402 <212> TYPE: DNA
 403 <213> ORGANISM: Artificial Sequence
 W--> 404 <220> FEATURE:
 405 <223> OTHER INFORMATION: Sequence of CA primer
 407 <400> SEQUENCE: 16
 E--> 409 cca cgt cct cct gcc cgc cgc 21←
 E--> 412 8

delete

*insert a hard
 return after nucleotide
 at location 48. Per
 1.822 of Sequence Rules,
 a maximum
 of 48
 triplets
 per line*

last sequence in submitted file

VERIFICATION SUMMARY

DATE: 10/10/2003

PATENT APPLICATION: US/09/786,926A

TIME: 10:55:40

Input Set : A:\pto.yf.txt

Output Set: N:\CRF4\10102003\I786926A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:283 W: Missing Blank Line separator, <220> field identifier
L:119 M:283 W: Missing Blank Line separator, <220> field identifier
L:150 M:283 W: Missing Blank Line separator, <220> field identifier
L:181 M:283 W: Missing Blank Line separator, <220> field identifier
L:267 M:283 W: Missing Blank Line separator, <220> field identifier
L:272 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:5
L:279 M:283 W: Missing Blank Line separator, <220> field identifier
L:284 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:6
L:291 M:283 W: Missing Blank Line separator, <220> field identifier
L:296 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:7
L:302 M:283 W: Missing Blank Line separator, <220> field identifier
L:307 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:8
L:314 M:283 W: Missing Blank Line separator, <220> field identifier
L:319 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:9
L:326 M:283 W: Missing Blank Line separator, <220> field identifier
L:331 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:10
L:337 M:283 W: Missing Blank Line separator, <220> field identifier
L:342 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:11
L:349 M:283 W: Missing Blank Line separator, <220> field identifier
L:354 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:12
L:362 M:283 W: Missing Blank Line separator, <220> field identifier
L:367 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:13
L:379 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:49 SEQ:14
L:387 M:283 W: Missing Blank Line separator, <220> field identifier
L:392 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:15
L:404 M:283 W: Missing Blank Line separator, <220> field identifier
L:409 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:16
M:254 Repeated in SeqNo=16
L:22 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (4) Counted (16)